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OM protein - nucleic search, using frame_plus_p2n model
Run on: December 13, 2002, 19:38:42 : Search time 100 seconds
(without alignments)
1301.067 Million cell updates/sec

Title: US-09-758-593A-1
Perfect score: 1693
Sequence: 1 MEDSEAVQATALIEQRQA.....NGLEPNDSGRETPQVPQAQ 329

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 355320 seqs, 197730502 residues

Total number of hits satisfying chosen parameters: 710640
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications, NA.*
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1693	100.0	1158	Sequence 48, Appl
2	1693	100.0	1158	Sequence 2, Appl
3	918	54.2	576	Sequence 3, Appl
4	790	46.7	569	Sequence 5, Appl

5	662	39.1	1889	9	US-09-974-298-182	Sequence 182, App
6	606	35.8	550	10	US-09-833-381-837	Sequence 837, Appl
7	442	26.1	253	10	US-09-758-593A-4	Sequence 4, Appl
8	437	25.8	315	10	US-09-758-593A-9	Sequence 9, Appl
9	332	19.6	207	10	US-09-758-593A-10	Sequence 10, Appl
10	297	17.5	255	10	US-09-758-593A-7	Sequence 7, Appl
11	292	17.2	275	10	US-09-758-593A-8	Sequence 8, Appl
12	276	16.3	330	10	US-09-758-593A-6	Sequence 6, Appl
13	249.5	14.7	4134	10	US-09-841-835-1	Sequence 1, Appl
14	249.5	14.7	4657	10	US-09-841-835-9	Sequence 9, Appl
15	247.5	14.6	3400	10	US-09-509-196A-1	Sequence 1, Appl
16	246	14.5	4491	10	US-09-841-835-7	Sequence 7, Appl
17	239.5	14.1	737	10	US-09-910-943-434	Sequence 434, App
18	239.5	14.1	744	9	US-09-938-842A-805	Sequence 805, App
19	235	13.9	1773	10	US-09-835-788A-7	Sequence 7, Appl
20	232.5	13.7	1299	10	US-09-908-711-12	Sequence 12, Appl
21	232	13.7	641	10	US-09-833-381-1141	Sequence 1141, Ap
22	225	13.3	2409	9	US-09-964-899-40	Sequence 40, Appl
23	219	12.9	1957	10	US-09-735-368-1	Sequence 1, Appl
24	219	12.9	2505	10	US-09-947-199-3	Sequence 3, Appl
25	219	12.9	3025	10	US-09-947-199-1	Sequence 1, Appl
26	217.5	12.8	5352	10	US-09-833-381-1027	Sequence 1027, Ap
27	217.5	12.8	5352	10	US-09-833-381-1028	Sequence 1028, Ap
28	214	12.6	5175	9	US-09-964-899-42	Sequence 42, Appl
29	212.5	12.6	2505	10	US-09-947-199-9	Sequence 9, Appl
30	212.5	12.6	3026	10	US-09-947-199-7	Sequence 7, Appl
31	212	12.5	1599	9	US-09-938-842A-1931	Sequence 1931, Ap
32	209	12.3	1356	10	US-09-815-925-7	Sequence 7, Appl
33	207	12.2	3000	10	US-09-728-952-29	Sequence 29, Appl
34	205.5	12.1	2826	10	US-09-728-952-30	Sequence 30, Appl
35	205	12.1	736	10	US-09-833-381-1150	Sequence 1150, Ap
36	200	11.8	2024	10	US-09-835-788A-3	Sequence 3, Appl
37	198.5	11.7	800	10	US-09-833-381-839	Sequence 839, App
38	198	11.7	990	10	US-09-884-870-3	Sequence 3, Appl
39	198	11.7	1538	10	US-09-884-870-1	Sequence 1, Appl
40	197	11.6	501	10	US-09-833-790-151	Sequence 151, App
41	196.5	11.6	1740	12	US-10-044-090-570	Sequence 570, App
42	195.5	11.5	948	9	US-09-938-842A-2359	Sequence 2359, Ap
43	195	11.5	747	10	US-09-908-805B-38	Sequence 38, Appl
44	195	11.5	1353	10	US-09-896-720-1	Sequence 1, Appl
45	194	11.5	1069	10	US-09-833-381-841	Sequence 841, App

ALIGNMENTS

RESULT 1
US-09-880-192-48
; Sequence 48, Application US/09880192
; Patent No. US20020077470A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Klingler, Tod M.
; APPLICANT: Azimzai, Yalda
; TITLE OF INVENTION: POLYNUCLEOTIDES ASSOCIATED WITH CARDIAC MUSCLE FUNCTION
; FILE REFERENCE: PB-0009-1 CIP
; CURRENT APPLICATION NUMBER: US/09/880,192
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PERL Program
; SEQ ID NO 48
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020077470A1 5578191CBI
US-09-880-192-48

Alignment Scores:
Pred. No.: 3.62e-169 Length: 1158
Score: 1693.00 Matches: 329
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-880-192-48 (1-1158)

Qy	1	MetGluAspSerGluAlaValGlnArgAlaThrAlaLeuIleGluGlnArgLeuAlaGln	20
Db	20	ATGAGGACTCCGAGCGGTGCAGAGGCCACAGCGCTCATCGAGCAGCGCTGGCACAG	79
Qy	21	GluGluGlnAsnGluLysLeuArgGlyAspThrArgGlnLysLeuProMetAspLeuLeu	40
Db	80	GAGGAGGAGATGAGAACTCCGAGGAGACACAGCGCAGAGCTGCCCATGGACTTCTGT	139
Qy	41	ValLeuGluAspGluLysHisGlyAlaGlnSerAlaAlaLeuGlnLysValLysGly	60
Db	140	GTGCTGGAGGATGAGAACACCGCGGCTCAGAGTGCAGCCCTGCAGAGGTGAAGGC	199
Qy	61	GlnGluArgValArgLysThrSerLeuAspLeuArgGluIleIleAspValGlyGly	80
Db	200	CAAGAGCGCTGCCAAGACGCTCCGTGCACCTCGCGGGAGATCATCGATGTGGCGGG	259
Qy	81	IleGlnAsnLeuIleGluLysMetLysValIleGluLysPheLeuAlaAspGly	140
Db	380	TTCTCTGAAGCTCGGTGAGGGGAAATGAAGGTCAITGAGAACTTCTTCGTGACGGG	439
Qy	141	GlySerAlaAspThrCysAspGlnPheArgThrAlaLeuHisArgAlaSerLeuGlu	160
Db	440	GGGTGAGCGGACACCTGGGACAGTTCGCTCGGACAGACCTGCACCGAGCTTCCCTGGAA	499
Qy	161	GlyHisMetGluIleGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAsp	180
Db	500	GGCCACATGGAAATCCTGGAGAGCTTCTAGATATGGGGCCACTGTGGACTTCCAGAT	559
Qy	181	ArgLeuAspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValVallys	200
Db	560	CGGCTGGACTGCACAGCATGCTGGGCTCCCGCGGGGCCACTTATAGAGTGTGTGAAA	619
Qy	201	LeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLysLeuSerThrProLeu	220
Db	620	CTTCTGCAAGCCATGGAGCAGACACCAATGTGAGGGATAAGCTGCTGAGCACCCCGCTG	679
Qy	221	HisValAlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeu	240
Db	680	CACGTGGCAGTCCGACAGGGCAGGTGGAGATGTGGAGCACTTCTATCCCTGGGCTG	739
Qy	241	GluIleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsn	260
Db	740	GAATATCAATGCCAGACAGGAGGAGGATGCTGCCCTGCATGACGCTGTGAGGCTCAAC	799
Qy	261	ArgTyrLysIleIleLysLeuLeuLeuHisGlyAlaAspMetMetThrLysAsnLeu	280
Db	800	CGCTACAAATCATCAACTGCTCTCCATGGGGCTGACATGATGACCAAGAACCTG	859
Qy	281	AlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHisAlaLeu	300
Db	860	GCAGGAAAGACCCGACGACCTGTGTGAGCTCTGCGAGGCTGATACCGCGGACGCTG	919
Qy	301	GluHisProGluProGlyAlaGluHisAsnGlyLeuGluGlyProAsnAspSerGlyArg	320
Db	920	GAGCATCTCTGAGCGGGGCTGAGCATAACGGGCTGGAGGGGCTTAATATAGTGGCGA	979
Qy	321	GluThrProGlnProValProAlaGln	329
Db	980	GAGACCCCTCAGCCTGTGCCAGCCCCAG	1006

RESULT 2

US-09-758-593A-2
; Sequence 2, Application US/09758593A
; Patent No. US20020127636A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein
; FILE REFERENCE: PC-0025 CIP
; CURRENT APPLICATION NUMBER: US/09/758,593A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020127636A1 5578191CBI
US-09-758-593A-2

Alignment Scores: 3,62e-169 Length: 1158
Pred. No.: 1693.00 Matches: 329
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 10

US-09-758-593A-1 (1-329) x US-09-758-593A-2 (1-1158)

Qy	1	MetGluAspSerGluAlaValGlnArgAlaThrAlaLeuIleGluGlnArgLeuAlaGln	20
Db	20	ATGAGGACTCCGAGCGGTGCAGAGGCCACAGCGCTCATCGAGCAGCGCTGGCACAG	79
Qy	21	GluGluGlnAsnGluLysLeuArgGlyAspThrArgGlnLysLeuProMetAspLeuLeu	40
Db	80	GAGGAGGAGATGAGAACTCCGAGGAGACACAGCGCAGAGCTGCCCATGGACTTCTGT	139
Qy	41	ValLeuGluAspGluLysHisGlyAlaGlnSerAlaAlaLeuGlnLysValLysGly	60
Db	140	GTGCTGGAGGATGAGAACACCGCGGCTCAGAGTGCAGCCCTGCAGAGGTGAAGGC	199
Qy	61	GlnGluArgValArgLysThrSerLeuAspLeuArgGluIleIleAspValGlyGly	80
Db	200	CAAGAGCGCTGCCAAGACGCTCCGTGCACCTCGCGGGAGATCATCGATGTGGCGGG	259
Qy	81	IleGlnAsnLeuIleGluLysMetLysValIleGluLysPheLeuAlaAspGly	100
Db	260	ATCCAGAACCTCATCGAGCTCGGAGAAACCGAAGCAGAACAGCGGACGCTCTGGCC	319
Qy	101	AlaSerHisGluProProGluProGluIleThrGlyProValAspGluGluThr	120
Db	320	GCCTCGCATGAGCCGCCCCAGAGCCCGGAGAGATCACTGGCCCTGTGGATGAGGAGAC	379
Qy	121	PheLeuLysAlaAlaValGluGlyLysMetLysValIleGluLysPheLeuAlaAspGly	140
Db	380	TTCTCTGAAGCTCGGTGAGGGGAAATGAAGGTCAITGAGAACTTCTTCGTGACGGG	439
Qy	141	GlySerAlaAspThrCysAspGlnPheArgThrAlaLeuHisArgAlaSerLeuGlu	160
Db	440	GGGTGAGCGGACACCTGGGACAGTTCGCTCGGACAGCACTGCACCGAGCTTCCCTGAA	499
Qy	161	GlyHisMetGluIleLeuGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAsp	180
Db	500	GGCCACATGGAAATCCTGGAGAGCTTCTAGATATGGGGCCACTGTGGACTTCCAGAT	559
Qy	181	ArgLeuAspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValVallys	200
Db	560	CGGCTGGACTGCACAGCATGCTGGGCTCCCGCGGGGCCACTTATAGAGTGTGTGAAA	619
Qy	201	LeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLysLeuSerThrProLeu	220

|||||
Db 620 CTTCTGCAAGGCATGGAGCAGACACCAATGTGAGGATAAAGCTGCTGAGCACCCCGCTG 679
QY 221 HisValAlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeu 240
Db 680 CACGTGGGAGTCCGACAGGCGAGGTGGAGATGTGGAGCACTTTCTATCCCTGGGCGCTG 739
QY 241 GluIleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsn 260
Db 740 GAAATCAATGCCAGAGACAGAGGAGGGATAGTCCCTGCATGACGCTGTGAGGCTCAAC 799
QY 261 ArgTyrLysIleLeuLysLeuLeuLeuHisGlyAlaAspMetMetThrLysAsnLeu 280
Db 800 CGCTACAAATCATCAAACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 859
QY 281 AlaGlyLysThrProThrAspLeuValGlnLeuThrGlnAlaAspThrArgHisAlaLeu 300
Db 860 GCAGAAAGACCCGACGAGCTGTGACAGTCTGCGAGGCTGATACCGGCGACGCCCTG 919
QY 301 GluHisProGluProGlyAlaGluHisAsnGlyLeuGluGlyProAsnAspSerGlyArg 320
Db 920 GAGCATCTGACCGGGGGCTGAGCATACGGGCTGGAGGGCCCTAATGATAGTGGCGA 979
QY 321 GluThrProGlnProValProAlaGln 329
Db 980 GAGACCCCTCAGCTGTGCCAGCCAG 1006

RESULT 3

US-09-758-593A-3

; Sequence 3, Application US/09758593A

; Patent No. US20020127636A1

; GENERAL INFORMATION:

; APPLICANT: Walker, Michael, G.

; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein

; FILE REFERENCE: PC-0025 CIP

; CURRENT APPLICATION NUMBER: US/09/758,593A

; CURRENT FILING DATE: 2001-06-11

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PERL Program

; SEQ ID NO 3

; LENGTH: 576

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20020127636A1 972118R6

US-09-758-593A-3

Alignment Scores:
Pred. No.: 4,3e-88 Length: 576
Score: 918.00 Matches: 187
Percent Similarity: 98.42% Conservative: 0
Best Local Similarity: 98.42% Mismatches: 1
Query Match: 54.22% Indels: 2
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-758-593A-3 (1-576)

QY 1 MetGluAspSerGluAlaValGlnArgAlaThrAlaLeuIleGluGlnArgLeuAlaGln 20
Db 10 ATGGAGGACTCCGAGGCGGTGCAGAGGGCCACAGCGCTCATCGAGCAGCGGCTGGCACAG 69
QY 21 GluGluGluAsnGluLysLeuArgGlyAspThrArgGlnLysLeuProMetAspLeuLeu 40
Db 70 GAGGAGGAGAATGAGAAATCCGAGGAGACCGACGCCCAAGCTGCCATGAGCTGCTG 129
QY 41 ValLeuGluAspGluLysHisGlyAlaGlnSerAlaAlaLeuGlnLysValLysGly 60
Db 130 GTGCTGGAGATGAGAGACCAACCGGGCTCAGATGTCAGCCCTCGAGAGGTGAGGGC 189
QY 61 GlnGluArgValArgLysThrSerLeuAspLeuArgArgGluIleLeuAspValGlyGly 80
Db 190 CAAGAGCGCTCGCAAGACGCTCCCTGGACCTGCGCGGGAGATCATCATGCTGGCGGG 249

QY 81 IleGlnAsnLeuIleGluLeuArgLysLysArgLysGlnLysLysArgAspAlaLeuAla 100
Db 250 ATCCAGAACCTCATGAGCTGGGAAGAACCGACAGCAAGACGCGACGCTCTGGCC 309
QY 101 AlaSerHisGluProProGluProGluGluIleThrGlyProValAspGluGluThr 120
Db 310 GCCTCGCATGAGCCGCCCCAGAGCCGAGGAGATCACTGGCCCTGTGATGAGGAGACC 369
QY 121 PheLeuLysAlaAlaValGluGlyLys-MetLysValIleGluLysPheLeuAlaAspG 140
Db 370 TTCTCTGAAAGCTGCGGTGGAGGGGAACATGAAGGTTCATTGAGAGCTTCTCTGCTGACGG 429
QY 140 VGLYSerAlaAspThrCysAspGlnPheArgArgThrAlaLeuHisArgAlaSerLeuG 160
Db 430 GGGGTGAGCCGACAGTGGCAGCCAGTTCGTCGGACAGCACGACCCGAGCTTCCCTGGA 489
QY 160 u-GlyHisMetGluIleLeuGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnA 180
Db 490 AGGGCCACATGGAATCTCTGGAGAAAGCTCTAGATAATGGGCCACTGTGGACTTCCAGG 549
QY 180 sArgLeuAspCysThrAlaMetHis 188
Db 550 ATCGGCTGAGCTGCACAGCCATGCAT 575

RESULT 4

US-09-758-593A-5/C

; Sequence 5, Application US/09758593A

; Patent No. US20020127636A1

; GENERAL INFORMATION:

; APPLICANT: Walker, Michael, G.

; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein

; FILE REFERENCE: PC-0025 CIP

; CURRENT APPLICATION NUMBER: US/09/758,593A

; CURRENT FILING DATE: 2001-06-11

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PERL Program

; SEQ ID NO 5

; LENGTH: 569

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20020127636A1 972118T6

US-09-758-593A-5

Alignment Scores:
Pred. No.: 1,21e-74 Length: 569
Score: 790.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.66% Indels: 0
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-758-593A-5 (1-569)

QY 181 ArgLeuAspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuValValLys 200
Db 567 CGGCTGAGCTGCACGCCATGTCATTTGGGCTGCCGGGGGCGCCACTTAGAGGTGTGAAA 508
QY 201 LeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeu 220
Db 507 CTTCTGCAAGGCATGGAGCAGACACCAATGTGAGGGATAAGCTGTGAGCACCCTGCTG 448
QY 221 HisValAlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeu 240
Db 447 CAGCTGGCAGTCCGGACAGCGAGGTGGAGATTGTGGACACTTTCTATCCCTGGGCGCTG 388
QY 241 GluIleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsn 260
Db 387 GAAATCAATGCCAGACAGACAGGAGGGGATGATCTGCTGATGACGCTGTGAGGCTCAAC 328
QY 261 ArgTyrLysIleIleLysLeuLeuLeuHisGlyAlaAspMetMetThrLysAsnLeu 280

Db	327	CGGTACAAATCATCAAACTGCTGCTCCTCATGGGCTGACATGATGACCAAGACCTG	268
Qy	281	AlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHisAlaLeu	300
Db	267	GCAGAAAGACCCGACGGACCTGGTGCAGCTCTGGCAGGCTGATACCCGCGACGCCCTG	208
Qy	301	GluHisProGluProGlyAlaGluHisAsnGlyLeuGluGlyProAsnAspSerGlyArg	320
Db	207	GAGCATCTGAGCGGGGCTGAGCATAAAGCGGCTGGAGGGGCTTAATGATAGTGGCGCA	148
Qy	321	GluThrProGlnProValProAlaGln	329
Db	147	GAGACCCCTCAGCCTGTGCCAGCCAG	121
RESULT 5			
US-09-974-298-182			
; Sequence 182, Application US/09974298			
; Patent No. US20020156263A1			
; GENERAL INFORMATION:			
; APPLICANT: Chen, Huel-Mei			
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER			
; FILE REFERENCE: PA-0037 P			
; CURRENT APPLICATION NUMBER: US/09/974,298			
; CURRENT FILING DATE: 2001-10-04			
; PRIOR APPLICATION NUMBER: 60/238,331			
; PRIOR FILING DATE: 2000-05-10			
; NUMBER OF SEQ ID NOS: 194			
; SOFTWARE: PERL Program			
; SEQ ID NO 182			
; LENGTH: 1889			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; NAME/KEY: misc.feature			
; OTHER INFORMATION: Incyte ID No. US20020156263A1 332919.4			
; NAME/KEY: unsure			
; LOCATION: 1882			
; OTHER INFORMATION: a, t, c, g, or other			
US-09-974-298-182			
Alignment Scores:			
Pred. No.:	1,77e-60	Length:	1889
Score:	662.00	Matches:	141
Percent Similarity:	67.92%	Conservative:	58
Best Local Similarity:	48.12%	Mismatches:	82
Query Match:	39.10%	Indels:	13
DB:	9	Gaps:	4
US-09-758-593A-1 (1-329) x US-09-974-298-182 (1-1889)			
Qy	14	IleGluGlnArgLeuAlaGlnGluGluAsnGluLysLeuArgGlyAspThrArgGln	33
Db	182	CTGGAAGAAGATGGCAATCTTACTTAGAAGACGAGGAGGATCTCAAGACACTTCTAGCC	300
Qy	34	-----LysLeuProMetAspLeuValLeuGluAspGluLysHisGlyAla	50
Db	241	CGAGACTATGACCTGCTTACTTAGAAGACGAGGAGGATCTCAAGACACTTCTAGCC	300
Qy	51	GlnSerAlaAlaLeu-----GlnLysValLysGlyGlnGluArg-----Val	64
Db	301	CACCCCTGTGACCCCTGGGGGCAACAGTGTGAAAGCGAACAACACGAGACGACAGCTC	360
Qy	65	ArgLysThrSerLeuAspLeuArgGluIleAspValGlyGlyIleGlnAsnLeu	84
Db	361	AAAAAGAAAAATCAACAAAGCTTGAAAATTTAGACAGACCTTGAATAATC	420
Qy	85	IleGluLeuArgLysLysGlnLysLysArgAspAlaLeuAlaAlaSerHisGlu	104
Db	421	ATTCAACTGAAGAAAGGAAAAATACAGGAAACTTAAAGTTCCAGTTCTAAAGGAA---	477
Qy	105	ProProGluProGluGluIleThrGlyProValAspGluGluThrPheLeuLysAla	124

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Db 61 CACCTTCTATCCCTGGGCTGAAATCAATCCAGAGACAGGAAGGGGATACTGCCCTG 120
Qy 254 HisAlaValArgLeuAsnArgTyrLysIleLeuLeuLeuLeuHisGlyAla 273
Db 121 CATGACGCTGTGAGGCTCAACCGCTACAAATCATCAAACTGCTCTCATGGGGCT 180
Qy 274 AspMetThrLysAsnLeuAlaGlyLysThrProThrAspLeuValGlnLeuTyrGln 293
Db 181 GACATGATGACCAAGAACCTGGCAGGAAGACCCGAGGACCTGGTGCACCTCTGGCAG 240
Qy 294 AlaAspThrArgHisAlaLeuGluHisProGluProGluProGluHisAsnGlyLeuGlu 313
Db 241 GCTGATACCCGCGACCGCTCGAGCATCTGAGCGGGGCTGAGCATAACGGGCTGGAG 300
Qy 314 GlyProAsnAspSerGlyArgGluThrProGlnProValProAlaGln 329
Db 301 GGGCCTAATGATAGTGGGCGAGAGACCCCTCAGGCTGTGCCAGGCCAG 348
RESULT 7
US-09-758-593A-4
; Sequence 4, Application US/09758593A
; Patent No. US20020127636A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein
; FILE REFERENCE: PC-0025 CIP
; CURRENT APPLICATION NUMBER: US/09/758,593A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 253
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020127636A1 4852018H1
US-09-758-593A-4
Alignment Scores:
Pred. No.: 1.58e-38 Length: 253
Score: 442.00 Matches: 83
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.11% Indels: 0
Gaps: 10
Db:
US-09-758-593A-1 (1-329) x US-09-758-593A-4 (1-253)
Qy 114 GlyProValAspGluGluThrPheLeuLysAlaAlaValGluGlyLysMetLysValIle 133
Db 3 GGCCCTGTGGATGAGGAGACCTCTGAAAGCTCGGTGGAGGGGAAATGAAGTCAAT 62
Qy 134 GluLysPheLeuAlaAspGlyGlySerAlaAspThrCysAspGlnPheArgArgThrAla 153
Db 63 GAGAAATTCCTGGCTGAGCGGGGGTCCACCCAGCAGCTCGGACCACTTCCTGCGGACACA 122
Qy 154 LeuHisArgAlaSerLeuGluGlyHisMetGluLeuLeuGluLysLeuLeuAspAsnGly 173
Db 123 CTGACCCAGAGCTCCCTGGAAGGCCACATGGAATCCCTGGAGAAGCTTCTAGATAATGGG 182
Qy 174 AlaThrValAspPheGlnAspArgLeuAspCysThrAlaMetHisTrpAlaCysArgGly 193
Db 183 GCCACTGTGGACTTCCAGGATCGGCTGGACTGGACGACCATGTCATTTGGGCGCTGCCGCGG 242
Qy 194 GlyHisLeu 196
Db 243 GGCCACTTA 251
RESULT 8
US-09-758-593A-9
; Sequence 9, Application US/09758593A
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; Patent No. US20020127636A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein
; FILE REFERENCE: PC-0025 CIP
; CURRENT APPLICATION NUMBER: US/09/758,593A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020127636A1 700188047H1
; LOCATION: 54, 80, 121
; OTHER INFORMATION: a, t, c, g, or other
US-09-758-593A-9
Alignment Scores:
Pred. No.: 7.11e-38 Length: 315
Score: 437.00 Matches: 91
Percent Similarity: 93.33% Conservative: 7
Best Local Similarity: 86.67% Mismatches: 7
Query Match: 25.81% Indels: 2
Gaps: 0
Db:
US-09-758-593A-1 (1-329) x US-09-758-593A-9 (1-315)
Qy 121 PheLeuLysAlaAlaValGluGlyLysMetLysValIleGluLysPheLeuAlaAspGly 140
Db 2 TTCCTGAAAGCAGCGGTGGAGGAAATCAAGTCAATGACAAGTACCTGGNAGACCGA 61
Qy 141 GlySerAlaAspThrCysAspGlnPheArgArgThrAlaLeuHisArgAlaSerLeuGlu 160
Db 62 GGTTCGGCAGACACCTGTATCAGTTCCTGCGGACAGCAGCTGCATCGGCTCCCTGGAN 121
Qy 161 GlyHisMetGluLeuGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAsp 180
Db 122 GGACACATGGAGATACTGGAGAAACTTCTGGAGAAATGGGCCACCGCTGCAGGAT 181
Qy 181 ArgLeuAspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValLys 200
Db 182 CGCTGGAGACTGCACAGCCATGCACCTGGGCTGCTGCGGAGGCCACCTGGAGGTGTGAA 241
Qy 201 LeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeu 220
Db 242 TC-TTGCAAGTCGGGGGGCCACACACCGACGCTGAGAGACAGCTATG-AGCACTCCCTG 299
Qy 221 HisValAlaValArg 225
Db 300 CATGTGGGCGTCCGT 314
RESULT 9
US-09-758-593A-10
; Sequence 10, Application US/09758593A
; Patent No. US20020127636A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein
; FILE REFERENCE: PC-0025 CIP
; CURRENT APPLICATION NUMBER: US/09/758,593A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 207
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; NAME/KEY: misc_feature
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; OTHER INFORMATION: Incyte ID No. US20020127636A1 700913268H1
US-09-758-593A-10

Alignment Scores:
Pred. No.: 4.42e-27 Length: 207
Score: 332.00 Matches: 62
Percent Similarity: 95.65% Conservatives: 4
Best Local Similarity: 89.86% Mismatches: 3
Query Match: 19.61% Indels: 0
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-758-593A-10 (1-207)

QY 242 ILeAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsnArg 261
Db 1 ATCAATCCCAAGACAGAGAGAGGGGAGAGTGCCTGCATGATCGCGTGCAGACTCAACCGC 60
QY 262 TyrlYsilelleLysLeuLeuLeuHisGlyAlaAspMetMetThrLysAsnLeuAla 281
Db 61 TACAANAATCATCAAACTGCTCTTGCATGGGCGACAGATGATGGCTAAGAATAATGGCG 120
282 GlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHisAlaLeuGlu 301
Db 121 GGAAGACCCCTACCGACCTGGTCCAGCTGTGGCAGCAGACACCCCGCATGCCCTGGAG 180
QY 302 HisProGluProGlyAlaGluHisAsn 310
Db 181 CACCTGAACCAAGTACAGACAGACAGAC 207

RESULT 10
US-09-758-593A-7
; Sequence 7, Application US/09758593A
; Patent No. US20020127636A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein
; FILE REFERENCE: PC-0025 CIP
; CURRENT APPLICATION NUMBER: US/09/758, 593A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020127636A1 700911986H1
US-09-758-593A-7

Alignment Scores:
Pred. No.: 2.8e-23 Length: 255
Score: 297.00 Matches: 65
Percent Similarity: 82.72% Conservatives: 2
Best Local Similarity: 80.25% Mismatches: 14
Query Match: 17.54% Indels: 0
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-758-593A-7 (1-255)

QY 1 MetGluAspSerGluAlaValGlnArgAlaThrAlaLeuGluGlnArgLeuAlaGln 20
Db 12 ATGGAGGGTCCCGAGGCTGTGCAGAGAGCCACAGAGCTCATCGACGCGCTTGCAG 71
QY 21 GluGluGluAsnGluLysLeuArgGlyAspThrArgGlnLysLeuProMetAspLeuLeu 40
Db 72 GAGGAAGAGACTGAGAACTTCGAGAGCCACTCTCTGGAGAGACCTCCATGGACATGCTA 131
QY 41 ValLeuGluAspGluLysHisGlyAlaGlnSerAlaAlaLeuGlnLysValLysGly 60
Db 132 GTGCTAGAGGACGAGAGCGCTCGGGTGCAGAGTCTCTGCTTTACAAAAGGTTAAGGC 191
QY 61 GlnGluArgValArgLysThrSerLeuAspLeuArgArgGluLeuLeuValGlyGly 80

Db 192 CAAGAGCGGTGCGCAAGACATCCCTGGACTTGCACGTGAGATCATTTGACGTGGCGG 251
QY 81 Ile 81
Db 252 ATC 254
RESULT 11
US-09-758-593A-8
; Sequence 8, Application US/09758593A
; Patent No. US20020127636A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein
; FILE REFERENCE: PC-0025 CIP
; CURRENT APPLICATION NUMBER: US/09/758, 593A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 8
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020127636A1 701144158H1
US-09-758-593A-8

Alignment Scores:
Pred. No.: 1.04e-22 Length: 275
Score: 292.00 Matches: 72
Percent Similarity: 82.61% Conservatives: 4
Best Local Similarity: 78.26% Mismatches: 14
Query Match: 17.25% Indels: 3
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-758-593A-8 (1-275)

QY 1 MetGluAspSerGluAlaValGlnArgAlaThrAlaLeuGluGlnArgLeuAlaGln 20
Db 5 ATGGAGGGTCCCGAGGCTGTGCAGAGAGCCACAGAGCTCATCGACGCGCTTGCAG 64
QY 21 --GluGluGluAsnGluLysLeuArgGlyAspThrArgGlnLysLeuProMetAspLeu 40
Db 65 TGAAGAGGAAGACTGAGAACTTCGAGAGCCACTCTCTGGGAAGAGCTCCATGGACATGC 124
QY 40 euValLeuGluAspGluLysHisGlyAlaGlnSerAlaAlaLeuGlnLysValLysG 60
Db 125 TAGTGCTAGAGGACGAGAGCGCT--GGGTGCAGAGTCTCTTTACAAAAGGTTAAGG 183
QY 60 lyGlnGluArgValArgLysThrSerLeuAspLeuArgArgGluLeuLeuAspValGlyG 80
Db 184 GCCAAGAGCGCGTGCAGAGACATCCCTGGACTTGGACGTGGACGTGAGATCATTTGACGTGGCG 243
QY 80 lytleGlnAsnLeuLeuGluLeuArgLysLys 90
Db 244 GGATCCAGAACTCATAGAACTGAGGAAAAA 275

RESULT 12
US-09-758-593A-6
; Sequence 6, Application US/09758593A
; Patent No. US20020127636A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein
; FILE REFERENCE: PC-0025 CIP
; CURRENT APPLICATION NUMBER: US/09/758, 593A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 330
; TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020127636A1 7350215H1
US-09-758-593A-6

Alignment Scores:
Pred. No.: 6,42e-21 Length: 330
Score: 276.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.30% Indels: 0
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-758-593A-6 (1-330)

QY 280 LeuAlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHisAla 299
DB 3 CTGGCAGGAAGAACCCCGACGACCTGGTGCAGCTTGGCAGGCTGATACCCGGCACGCC 62
QY 300 LeuGluHisProGluProGlyAlaGluHisAsnGlyLeuGluGlyProAsnAspSerGly 319
DB 63 CTGGAGCATCTCGACCGCGGGGCTGAGCATACGCGGTGGAGGGGCTTAATCATAGTGGG 122
QY 320 ArgGluThrProGlnProValProAlaGln 329
DB 123 CGAGAGACCCCTCAGCCTGTGCGACGCCAG 152

RESULT 13

US-09-841-835-1
Sequence 1, Application US/09841835
Patent No. US20020076795A1
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4134 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

US-09-841-835-1
Alignment Scores:
Pred. No.: 1,2e-16 Length: 4134
Score: 249.50 Matches: 91
Percent Similarity: 35.73% Conservative: 33
Best Local Similarity: 26.22% Mismatches: 110
Query Match: 14.74% Indels: 113
DB: 10 Gaps: 9
US-09-758-593A-1 (1-329) x US-09-841-835-1 (1-4134)
QY 40 LeuValLeuGluAspGluLysHis-----HisGlyAlaGlnSerAlaLaLeuGln 56
DB 1455 TTGACTTATGAATTTAAAGTCTATTCTTTACTACAGCAGCCAGAGAGACGACTTAGCT 1514
QY 57 LysValLysGlyGlnGluArgValArgLysThrSerLeuAspLeuArgGluLeuLe 76
DB 1515 AAAGTTAAA-----AAACA-----CTCGCTCTGGAAATCAT 1547
QY 77 AspValGlyGlyLeuGlnAsn-----LeuIleGluLeuArg 88
DB 1548 AATTTCAACAACCGCAGCTCTCATGAAACAGCAGCTCCTGTCTGTCTCTCTGCAT 1607
QY 89 LysLysArgLysGln-----Lys 94
DB 1608 CCCAAACGTAAACAAGTGACAGAAATGTTACTTAGAAAAGGAGCAATGTTAATGAANA 1667
QY 95 LysArgAspAlaLeuAlaSerHisGluProProGluProGluGluLeuThrGly 114
DB 1668 AATAAAGATTTCATGACTCCCTGCAT----- 1694
QY 115 ProValAspGluGluThrPheLeuLysAlaAlaValGluGlyLysMetLysValIleGlu 134
DB 1695 -----GTTGCAGCCGAAAGAGCCCATTAATGATGTCATGGA 1730
QY 135 LysPheLeuAlaAspGlyGlySerAlaAspThrCysAspGlnPheArgArgThrAlaLeu 154
DB 1731 GTTCTGCATAAGCATGGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATG 1790
QY 155 HisArgAlaSerLeuGluGlyHisMetGluIleLeuGluLysLeuAspAsnGly 173
DB 1791 CATAGAGCCGCTAGCAGGCCACCTGCAGACCTGCGCCTCTCTGCTGAGTACGGCTCT 1850
QY 173 ----- 173
DB 1851 GACCCCTCCATCATCTCTTACAAGCTTTCACAGCAGCAGATGGGCAATGAAGCAGTG 1910
QY 174 -----AlaThrValAspPheGln----- 179
DB 1911 CAGCAGATTCTGAGTGAGAGTACACCTATACGTACTTCTGATGTTGATGTTATCGACTT 1970
QY 180 -----AspArgLeu 182
DB 1971 GAGGCATCTAAAGCTGGAGACTTGGAACTGTGAAGCAACTTTGACGCTCTCAAAATGTG 2030
QY 183 AspCys-----ThrAlaMetHisTrpAlaCysArgGlyGly 194
DB 2031 AATGTGAGAGACTTAGAGCGCGCGCATTCACGCCCTTACACTTCGACGAGGCTACAAC 2090
QY 195 HisLeuGluValLysLeuGlnSerHisGlyAlaAspThrAsnValArgAspLys 214
DB 2091 CGCGTCTCTGTGTAGAGTACCTGTACACCGGTGCGGATGTCATGCCAAGACAAG 2150
QY 215 LeuLeuSerThrProLeuHisValAlaValArgThrGlyGlnValGluLeuHis 234
DB 2151 GGTGGCTTGGTGCCTTCATAATGCTGTTTCATATGGACACTATCAGGTGGCTGAGCTT 2210
QY 235 PheLeuSerLeuGlyLeuGluLeuAsnAlaArgAspArgGlyAspThrAlaLeuHis 254
DB 2211 TTAGTAAGGCATGGGGCTTCTGTGTCATATGGGAGCTTATGGAAATTTACCCCTCTCCAT 2270
QY 255 AspAlaValArgLeuAsnArgTyrLysIleLeuLeuLeuLeuHisGlyAlaAsp 274

Search completed: December 14, 2002, 01:40:35
Job time : 108 secs

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QY 180 -----AspArgLeu 182
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6..2855
US-09-196-387-9
Alignment Scores:
Pred. No.: 1.83e-17 Length: 4657
Score: 249.50 Matches: 91
Percent Similarity: 35.73% Conservative: 33
Best Local Similarity: 26.22% Mismatches: 110
Query Match: 14.74% Indels: 113
Gaps: 9
US-09-758-593A-1 (1-329) x US-09-196-387-9 (1-4657)
QY 40 LeuValLeuGluAspClnLysHis-----HisGlyAlaClnSerAlaAlaLeuGln 56
Db 1455 TTGACTTATGAATTTAAAGGTCACTTTTACTACAAGCAGCCAGAGAGCAGACTTAGCT 1514
QY 57 LysValLysGlyGlnGluArgValArgLysThrSerLeuAspLeuArgGluIleIle 76
Db 1515 AAAGTTAAA-----AAACA-----CTCGCTCTGGAATCAT 1547
QY 77 AspValGlyGlyIleGlnAsn-----LeuIleGluLeuArg 88
Db 1548 AATTTCAAAACAACCGCAGTCTCATGAAACAGCAGCTGCTGTGCGCTCTCTGCAT 1607
QY 89 LysLysArgLysGln-----Lys 94
Db 1608 CCCAACGTAACCAAGTGAAGTACAGAACTTGTACTTAGAAAAGGACAAATGTTAATGAAAA 1667
QY 95 LysArgAspAlaLeuAlaSerHisGluProProGluProGluGluIleThrGly 114
Db 1668 AATAAGATTTCATGACTCCCTGCAT----- 1694
QY 115 ProValAspGluThrPheLeuLysAlaAlaValGluGlyLysMetLysValIleGlu 134
Db 1695 -----GTTGCGCGCGAAAGACCCATAATGATGTCATGGAA 1730
QY 135 LysPheLeuAlaAspGlyGlySerAlaAspThrCysAspClnPheArgArgThrAlaLeu 154
Db 1731 GTTCTGCATTAAGCATGGCCCAAGATGAATGCATGACCCCTGGTCAGACTGCTTTG 1790
QY 155 HisArgAlaSerLeuGluGlyHisMetGluIleLeuGluLysLeuLeuAspAsnGly 173
Db 1791 CATAGAGCGCGCTAGCAGCGCCACCTGCGAGACCTGCGGCTCTGCTGAGTTACGGCTCT 1850
QY 173 ----- 173
Db 1851 GACCCCTCATCATCTCTTACAAGCTTTCACAGCAGCAGATGGCAATGAAGCAGTG 1910
QY 174 -----AlaThrValAspPheGln----- 179
Db 1911 CAGCAGATTCTCAGTGAGAGTACACCTATACGTACTTCTCTGATGTTGATTTATCGACTTAA 1970
QY 180 -----AspArgLeu 182
Db 1971 GAGGCATCTAAAGCTGGAGACTTGGAAACTGTGAAGCAACTTTGACGCTCTCAAAATGTG 2030
QY 183 AspCys-----ThrAlaMetHisTrpAlaCysArgGlyGly 194
Db 2031 AATTGTAGAGACTTAGAGGCGCGCATTCACGCCCTTACACTTCCGACAGGCTACAAC 2090
QY 195 HisLeuGluValValLysLeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLys 214
Db 2091 CGCGTGTCTGTTGTAGAGTACCTGCTACACCGGTGCGGATGCTCCCAAGACAAG 2150
QY 215 LeuLeuSerThrProLeuHisValAlaValArgThrGlyGlnValIleValGluHis 234
Db 2151 GGTGCTTGGTCCCTTCATGATGCTGCTCATATGACATGATGAGGTGCTGAGCTT 2210
QY 235 PheLeuSerLeuGlyLeuGluIleAsnAlaArgAspArgGluGlyAspThrAlaLeuHis 254
Db 2211 TTAGTAAGGCATGGGGCTTCTGCAATGTGGCGGACTTATGGAATTTTACCCCTCTCCAT 2270
QY 255 AspAlaValArgLeuAsnArgTyrLysIleIleLysLeuLeuLeuHisGlyAlaAsp 274
Db 2271 GAAGCAGCAGCTAAAGGAAGTATGAATCTGCAAGCTCTTTTAAACATGGAGCAGAT 2330
QY 275 MetMetThrLysAsnLeuAlaGlyLysThrProThrAspLeuValClnLeuTrpGlnAla 294
Db 2331 CCAACTAAAGAACACAGAGATGAAATACACCTTTGGATTTGGTAAAGGAGGAGACACA 2390
QY 295 AspThrArgHisAlaLeuGlu 301
Db 2391 GATATTCAGGACTTACTGAAA 2411
RESULT 3
US-09-196-387-9
; Sequence 9, Application US/09196387
; Patent No. 627613
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,387
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,225
; FILING DATE: June 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4657 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6..2855
US-09-196-387-9
Alignment Scores:
Pred. No.: 1.83e-17 Length: 4657
Score: 249.50 Matches: 91
Percent Similarity: 35.73% Conservative: 33
Best Local Similarity: 26.22% Mismatches: 110
Query Match: 14.74% Indels: 113
Gaps: 9
US-09-758-593A-1 (1-329) x US-09-196-387-9 (1-4657)
QY 40 LeuValLeuGluAspClnLysHis-----HisGlyAlaClnSerAlaAlaLeuGln 56
Db 1455 TTGACTTATGAATTTAAAGGTCACTTTTACTACAAGCAGCCAGAGAGCAGACTTAGCT 1514
QY 57 LysValLysGlyGlnGluArgValArgLysThrSerLeuAspLeuArgGluIleIle 76
Db 1515 AAAGTTAAA-----AAACA-----CTCGCTCTGGAATCAT 1547
QY 77 AspValGlyGlyIleGlnAsn-----LeuIleGluLeuArg 88
Db 1548 AATTTCAAAACAACCGCAGTCTCATGAAACAGCAGCTGCTGTGCGCTCTCTGCAT 1607
QY 89 LysLysArgLysGln-----Lys 94
Db 1608 CCCAACGTAACCAAGTGAAGTACAGAACTTGTACTTAGAAAAGGACAAATGTTAATGAAAA 1667
QY 95 LysArgAspAlaLeuAlaSerHisGluProProGluProGluGluIleThrGly 114
Db 1668 AATAAGATTTCATGACTCCCTGCAT----- 1694
QY 115 ProValAspGluThrPheLeuLysAlaAlaValGluGlyLysMetLysValIleGlu 134
Db 1695 -----GTTGCGCGCGAAAGACCCATAATGATGTCATGGAA 1730
QY 135 LysPheLeuAlaAspGlyGlySerAlaAspThrCysAspClnPheArgArgThrAlaLeu 154
Db 1731 GTTCTGCATTAAGCATGGCCCAAGATGAATGCATGACCCCTGGTCAGACTGCTTTG 1790
QY 155 HisArgAlaSerLeuGluGlyHisMetGluIleLeuGluLysLeuLeuAspAsnGly 173
Db 1791 CATAGAGCGCGCTAGCAGCGCCACCTGCGAGACCTGCGGCTCTGCTGAGTTACGGCTCT 1850
QY 173 ----- 173
Db 1851 GACCCCTCATCATCTCTTACAAGCTTTCACAGCAGCAGATGGCAATGAAGCAGTG 1910
QY 174 -----AlaThrValAspPheGln----- 179
Db 1911 CAGCAGATTCTCAGTGAGAGTACACCTATACGTACTTCTCTGATGTTGATTTATCGACTTAA 1970
QY 180 -----AspArgLeu 182
Db 1971 GAGGCATCTAAAGCTGGAGACTTGGAAACTGTGAAGCAACTTTGACGCTCTCAAAATGTG 2030
QY 183 AspCys-----ThrAlaMetHisTrpAlaCysArgGlyGly 194
Db 2031 AATTGTAGAGACTTAGAGGCGCGCATTCACGCCCTTACACTTCCGACAGGCTACAAC 2090
QY 195 HisLeuGluValValLysLeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLys 214
Db 2091 CGCGTGTCTGTTGTAGAGTACCTGCTACACCGGTGCGGATGCTCCCAAGACAAG 2150
QY 215 LeuLeuSerThrProLeuHisValAlaValArgThrGlyGlnValIleValGluHis 234
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Db 2151 GGTGGCTTGGTGGCCCTTCAATGCTTTCATATGACACACTAGAGTGGCTGAGCTT 2210
Qy 235 PheLeuSerLeuGluLeuAlaAsnAlaArgPheGluGlyAspThrAlaLeuHis 254
Db 2211 TTAGTAAGGCGATGGCTTCTGTCATATGGCGGACTTATGGAATTTACCCCTCTCCAT 2270
Qy 255 AsnAlaValArgLeuAsnArgTyrLysIleLeuLysLeuLeuHisGlyAlaAsp 274
Db 2271 GAAGCAGCAGCTAAGGAAAGTATGAATCTGCAAGCTCTCTTTTAAACATGGAGCAGAT 2330
Qy 275 MetMetThrLysAsnLeuAlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAla 294
Db 2331 CCAACTAAAGACACAGATGGAATACACCTTTGGATTGGTAAAGGAGGAGACACA 2390
Qy 295 AspThrArgHisAlaLeuGlu 301
Db 2391 GATATTCAGGACTTACTGAAA 2411

RESULT 4

US-09-196-387-7
Sequence 7, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 6..2027
US-09-196-387-7

Alignment Scores:
Pred. No.: 4,23e-17 Length: 4491
Score: 246.00 Matches: 82
Percent Similarity: 36.00% Conservative: 35

Best Local Similarity: 25.23% Mismatches: 102
Query Match: 14.53% Indels: 106
DB: Gaps: 7
US-09-758-593A-1 (1-329) x US-09-196-387-7 (1-4491)
Qy 64 ValArgLysThrSerLeuAspLeuArg---ArgGluIleIleAspValGlyGlyIleGln 82
Db 2295 ATACGTACTTCTGATCTTGTATGACTTAAAGCCACTTAAAGCTGGAGACTTTGGAA 2354
Qy 83 AsnLeuIleGluLeuArgLysLysGlnLysLysArgAspAlaLeuAlaSer 102
Db 2355 ACTGTGAAGCAACTTGCAGCTCTCAAAATGGAATTTAGAGAC---TTAGAGGCCGG 2411
Qy 103 HisGluProProGluProGluGluThrGlyProValAspGluGluThrPheLeu 122
Db 2412 CATTCACGCC---TTACAC 2429
Qy 123 LysAlaAlaValGluGlyLysMetLysValIleGluLysPheLeuAlaAspGlyGlySer 142
Db 2430 TTCGACGAGGCTACAAACCGCTGTCTGTGTAGAGTACCTGTACACACCGTCCGAT 2489
Qy 143 AlaAspThrCysAspGlnPheArgArgThrAlaLeuHisArgAlaSerLeuGluGlyHis 162
Db 2490 GTCCATGCCAAAGACAAAGGCTGGTGGTCCCTTCATAATGCCTGTTCATATGGACAC 2549
Qy 163 MetGluIleLeuGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAspArgLeu 182
Db 2550 TATGAGGTGGCTGAGCTTTTGTAGTGGCATGGGCTTCTCTCAATGTGGCGGACTTATGG 2609
Qy 183 AspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLysLeuLeu 202
Db 2610 AAATTACCCCTCTCCATGAAGCAGCAGCTAAAGAAAGTATGAAATCTCAAGCTCTT 2669
Qy 203 GlnSerHisGlyAla--- 207
Db 2670 TTAACACATGGAGCAGATCCAACTAAAGAACACAGAGATGGAATACACCTTTGGATTGG 2729
Qy 208 ---AspThrAsnValArgAspLysLeuLeu--- 216
Db 2730 GTAAAGGAAGGAGACACAGATATTTCAGACTTACTGAAAGGGATGCTGCTTTGTTGGAT 2789
Qy 216 --- 216
Db 2790 GCTGCCAAGAAAGGCTGCTGGCAAGAGTGCAGAAGCTGTATACCCAGAGATATCAAC 2849
Qy 217 ---SerThrProLeuHisValAlaValArgThrGlyGln 228
Db 2850 TGCAGACACACCCAGGCGCAGAAATTCACCCCTCTGCACCTGGCAGCAGGCTATAATAC 2909
Qy 229 ValGluIleValGluHisPheLeuSerLeuGluLeuLeuAsnAlaArgAspArgGlu 248
Db 2910 CTGGAAGTAGCTGAATATCTTCTAGAGCATGGAGCTGTATGTTATGCCAGGACAAAGGT 2969
Qy 249 Gly--- 249
Db 2970 GGTTTAATTCCTTCATATGCGGCATCTTATGGGCATGTTGACATAGCGGCTTTATTG 3029
Qy 250 ---AspThrAlaLeuHisAsp 255
Db 3030 ATAAATACACACGTGTGTAAATGCAACAGATAAGTGGGGGTTTACTCCCTCCATGAA 3089
Qy 256 AlaValArgLeuAsnArgTyrLysIleLeuLysLeuLeuHisGlyAlaAspMet 275
Db 3090 GCAGCCAGAAAGGAGGACGACGCTGTGCCCTCTCTCTAGCGCATGGTGGCAGACCCC 3149
Qy 276 MetThrLysAsnLeuAlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAsp 295
Db 3150 ACCATGAAGAACAGGAGGACCGCTCTGATCTGGCA-----ACAGCTGAC 3200
Qy 296 ThrArgHisAlaLeu 300
Db 3201 GATATCAGAGCTTTG 3215

Db	2017	CGCGATACCCAAAGCGACAGCATTTCAACACCTTTACATTTTATAGCAGCTGGTTATATAAATTTA	2075
Qy	230	GLuileValcIuHisPheLeuSerLeuGlyLeuGluIleAsnAlaAArgAspArgGluGly	249
Db	2077	GAAGTTGCAGAGTATTGTTTACAACACGAGCTGATGTGAATGCCAAGACAAGGAGGA	2136
Qy	249	-----	249
Db	2137	CTTATTCTTTACATAATGCAGCATTTACGGCGATGTAGATGTAGCAGCTCTACTAATA	2196
Qy	250	-----AspThrAlaLeuHisAspAla	256
Db	2197	AAGTATAATGCATGTCTCAATGCCAGGACAAATGGGCTTTCACACCTTTCACGAAGCA	2256
Qy	257	ValArgLeuAsnArgTyrLysIleIleLysLeuLeuLeuHisGlyAlaAspMetMet	276
Db	2257	GCCCAAAAGGACGAACACAGCTTTGTGCTTTGKTGTAGCCCATGGAGCTGACCCGACT	2316
Qy	277	ThrLysAsnLeuAlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThr	296
Db	2317	CTTTAAAAANTCAGGAAGACAAACACCTTTAGATTAGTT-----TCAGCGGATGAT	2367
Qy	297	ArgHisAlaLeu-----GluHispro	303
Db	2368	GTCAAGCGCTCTTGACAGCAGCATGCCCCCATCTGCTCTGCCCTCTTTGTACAAGCCT	2427
Qy	304	Glu-----ProGlyAlaGluHisAsnGlyLeuGluGlyProAsn	316
Db	2428	CAAGTGTCAATGGTGTGAGAAGCCAGGAGCACTGCGCATGCTCTC-----	2475
Qy	317	AspSerGlyArgGluThrProGlnProValProAla	328
Db	2476	TCTTCAGGTCCTACTAGCCCATCAAGCCCTTCTGCA	2511
RESULT 6			
US-09-350-982C-3			
: Sequence 3, Application US/09350982C			
: Patent No. 6455290			
: GENERAL INFORMATION:			
: APPLICANT: Berthelsen, Jens			
: APPLICANT: Toma, Salvatore			
: APPLICANT: Isacchi, Antonella			
: TITLE OF INVENTION: Tankyrase Homolog Protein(THP), Nucleic Acids, and			
: TITLE OF INVENTION: Same			
: FILE REFERENCE: PHRM-0043			
: CURRENT APPLICATION NUMBER: US/09/350,982C			
: CURRENT FILING DATE: 1999-07-09			
: NUMBER OF SEQ ID NOS: 10			
: SOFTWARE: PatentIn version 3.0			
: SEQ ID NO 3			
: LENGTH: 4512			
: TYPE: DNA			
: ORGANISM: Artificial			
: FEATURE:			
: OTHER INFORMATION: PCR Primers			
: NAME/KEY: misc.feature			
: LOCATION: (1124)..(1124)			
: OTHER INFORMATION: n is any nucleic acid			
: NAME/KEY: misc.feature			
: LOCATION: (2672)..(2672)			
: OTHER INFORMATION: n is any nucleic acid			
US-09-350-982C-3			
Alignment Scores:			
Pred. No.:	7.09e-17	Length:	4512
Score:	244.00	Matches:	80
Percent Similarity:	35.26%	Conservative:	30
Best Local Similarity:	25.64%	Mismatches:	88
Query Match:	14.41%	Indels:	114
DB:	4	Gaps:	7
US-09-758-593A-1 (1-329) x US-09-350-982C-3 (1-4512)			

Qy 124 AlaAlaValGluGlyLysMetLysValIleGluLysPheLeuAlaAspGlyGlySerAla 143
Db 1619 GCAGCTGGGTATAACAGAGTCCGGTGGTGAATATCTGTACAGCATGGAGCTGATGTG 1678
Qy 144 AspThrCysAspGlnPheArgThrAlaLeuHisArgAlaSerLeuGluGlyHisMet 163
Db 1679 CATGCTAAAGATAAAGRRGSCCTTGCTACCTTGGCAATGCTGCTTCTTATGGACATAT 1738
Qy 164 GluIleLeuGluLysLeuLeuAspGlnGlyAlaThrValAspPheGlnAspArgLeuAsp 183
Db 1739 GAAGTGTGAGAACTCTTGTGTTAAACATGAGCAGCTAGTAAATGATGATTTATGCAAA 1798
Qy 184 CysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLysLeuGln 203
Db 1799 TTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGAATTTGCAAACTTCTGCTC 1858
Qy 204 SerHisGlyAla----- 207
Db 1859 CAGCATGTTGAGACCCCTACAAAAAAGAGGATGGAATCTCTCTTGGATCTTGT 1918
Qy 208 -----AspThrAsnValArgAspLysLeu----- 216
Db 1919 AAAGATGAGATACAGATATTCAAGATCTGCTTAGGGGAGATGCGCTTTGCTAGATGCT 1978
Qy 216 ----- 216
Db 1979 GCCAAGAAGAGTGTGTTAGCCAGAGTGAAGAGTGTCTCTCTGTGATAATGTAATGTC 2038
Qy 217 -----SerThrProLeuHisValAlaValArgThrGlyGlnVal 229
Db 2039 CCGCATACCCRAAGCAGACATTCACACCTTTACATTTAGCAGCTGTTATATAATTTA 2098
Qy 230 GluIleValGluHisPheLeuSerLeuGluLeuAsnAlaArgAspArgGly 249
Db 2099 GAAGTTGAGAGTATTGTTTACACAGCGAGCTGATGTGAATGCCACAGACAAAGGAGGA 2158
Qy 249 ----- 249
Db 2159 CTTATTCCTTTACATAATGACCATCTTACGGGATGTAGATGTAGCAGCTCTACTAATA 2218
Qy 250 -----AspThrAlaLeuHisAspAla 256
Db 2219 AAGTATAATGCATGTCTCAATGCCAGCGAATAATGGCTTTTCCACCTTTTGACCAAGCA 2278
Qy 257 ValArgLeuAsnArgTyrLysIleIleLysLeuLeuHisGlyAlaAspMetMet 276
Db 2279 GCCCAAAAGGGAGCAGACAGCTTTGCTGCTGCTAGCCATGGAGCTGACCCGACT 2338
Qy 277 ThrLysAsnLeuAlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThr 296
Db 2339 CTTAAAAATCAGGAAGGACAAACACCTTTAGATTAGTT-----TCACCGGATGAT 2389
Qy 297 ArgHisAlaLeu-----GluHisPro 303
Db 2390 GTCAGGCTCTTCTGACAGCAGCATGCCCATCTGCTCTGCCCTCTTGTTTACAGGCT 2449
Qy 304 Glu-----ProGlyAlaGluHisAsnGlyLeuGluGlyProAsn 316
Db 2450 CAAGTCTCAATGGTGTGAGAGCCCGAGGACCATGCGAGTCTCTC----- 2497
Qy 317 AspSerGlyArgGluThrProGlnProValProAla 328
Db 2498 TCTTCAGGTCCTTCTAGCCCATCAAGCCCTTTCTGCA 2533

RESULT 7

US-09-082-059-1
; Sequence 1, Application US/09082059A
; Patent No. 6225086
; GENERAL INFORMATION:
; APPLICANT: Morrow, Jon S.
; APPLICANT: Devarajan, Prasad
; TITLE OF INVENTION: No. 6225086el Ankyrin Proteins and a Method for Their Identificad

; FILE REFERENCE: 44574-5002-US
; CURRENT APPLICATION NUMBER: US/09/082,059A
; CURRENT FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: 60/047356
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3454

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (131)..(3394)
; OTHER INFORMATION: DNA/protein segment- human kidney Ankyrin G119
US-09-082-059-1

Alignment Scores: 2.19e-15 Length: 3454
Pred. No.: 229.00 Matches: 57
Score: 229.00 Conservative: 32
Percent Similarity: 50.00% Mismatches: 87
Best Local Similarity: 32.02% Indels: 2
Query Match: 13.53% Gaps: 0
DB:

US-09-758-593A-1 (1-329) x US-09-082-059-1 (1-3454)

Qy 124 AlaAlaValGluGlyLysMetLysValIleGluLysPheLeuAlaAspGlyGlySerAla 143
Db 212 GCCTGCAAGAGTAATCAATTAAGTAATGAACTCTCTTGAACACGGTGCATCCATC 271
Qy 144 AspThrCysAspGlnPheArgThrAlaLeuHisArgAlaSerLeuGluGlyHisMet 163
Db 272 CAAGCTGTACCGAGTCGGGCTTACCCCAATCATCTGCTGCTTCATGGGCGATGA 331
Qy 164 GluIleLeuGluLysLeuLeuAspGlnGlyAlaThrValAspPheGlnAspArgLeuAsp 183
Db 332 AATATTGTATCACAACTAATGTCATCATGGAGCTTACCAACACCCCAATGTGAGAGGA 391
Qy 184 CysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLysLeuGln 203
Db 392 GAACAGCAGCTGCACATGGCAGCTCGTCCGCCCAAGCTGAAGTTGTGCGTATCTGGA 451
Qy 204 SerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeuHisValAla 223
Db 452 CAAGCAGGAGCTCAGGTAGAGCTAAAGCTAAAGATGACCAACACCCACTCCACATTTCA 511
Qy 224 ValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeuGluIleAsn 243
Db 512 GCCGACTGGGGAAGCAGCATAGTACACAGCTGTTGCGAGCAAGGGGCTCTCCAAAT 571
Qy 244 AlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsnArgTyrLys 263
Db 572 GCAGCCCAACTCTGGGTACACCCCACTTCCACTTTCCGCCCGAGAGGGCGATGAGGAT 631
Qy 264 IleIleLysLeuLeuLeuHisGlyAlaAspMetMetThrLysAsnLeuAlaGlyLys 283
Db 632 GTGGCGCGTCTCTTTGGATCATGGAGCTCTTTATCTATATAACAACAAGAGGATTT 691
Qy 284 ThrProThrAspLeuVal--GlnLeuTrpGlnAlaAspThrArgHisAla 299
Db 692 ACTCTCTTCTATGCGCAGCAAAATATGAAAGCTTGAAGTCGCAATCT 741

RESULT 8

US-08-484-575A-5
; Sequence 5, Application US/08484575A
; Patent No. 5925358
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran and David E. Junker
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White


```

; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,575A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELEPHONE: (212)278-0450
; TELEFAX: (212)391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2849 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 300..1568
; NAME/KEY: CDS
; LOCATION: complement (1685..2848)
;
; US-08-484-575A-5
;
; Alignment Scores:
; Pred. No.: 2,74e-15 Length: 2849
; Score: 227.00 Matches: 68
; Percent Similarity: 44.44% Conservative: 48
; Best Local Similarity: 26.05% Mismatches: 99
; Query Match: 13.41% Indels: 46
; DB: 2 Gaps: 7
;
; US-09-758-593A-1 (1-329) x US-08-484-575A-5 (1-2849)
;
; QY 66 LysThrSerLeuAspLeuArgGluIlelle-----AspValGlyGlyIleGlnAsn 83
; DB 297 AAAATGCTGTTGATTTGGCGTACAGAAATCTATTCGGGTGATATATCCCTAGTAGAAAAA 356
;
; QY 84 LeuIleGluLeuArgLysLysArgLysGlnLysLysArgAspAlaLeuAlaSerHis 103
; DB 357 CTATA-----AGATAAAGGTAATTCGATCAATATATCT--- 392
;
; QY 104 GluProProGluProGluIleThrGlyProValAspGluGluThrPheLeuLys 123
; DB 393 -----GTAGAGGAACACAACTCCGTTA-----ATAGAC 422
;
; QY 124 AlaAlaValGluGlyLysMetLysValIleGluLysPheLeuAlaAspGlyGlySerAla 143
; DB 423 GCTATAAGAACCGGAATGCCAAAATAGTAGAACTATTATCAAGCAGCGGCGGAAGTT 482
;
; QY 144 AspThrCysAsp---GlnPheArgArgThrAlaLeuHisArgAlaSerLeuGluGlyHis 162
; DB 483 AATCATGTAATTAATAAATTCCTAATCCCTTGTTAACAGCTATCAAAATAGGATCACAC 542
;
; QY 162 ----- 162
;
; DB 543 GATATAGTAAACTGCTGTTGATTAAACGGAGTTGATCTTCTATTTCGCCAGTCCCTGCC 602
;
; QY 163 -----MetGluIleLeuGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAsp 180
; DB 603 ATAAATAAGAAATGATAAAACTATATTAGTAGTGGTGTGAAAGTAAACACAAAAAT 662

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QY 181 ArgLeuAspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLys 200
; DB 663 GCTAAATCTAAAACTTCTTGCAATACGGGATTAAGAAATAAGACTTAGAGGTTATCAAA 722
;
; QY 201 LeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeu 220
; DB 723 ATGCTTTTGGAGTATGAGCTGATGTTAATAATAAAGATGATAACATATGTTATCTATA 782
;
; QY 221 HisValAlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeu 240
; DB 783 CACATAGCTACTAGGAGTAATTCATATGAATCATATAAAATTACTATTAGAAAAAGTGCT 842
;
; QY 241 GluIleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsn 260
; DB 843 TATGCAACGCTAAAGACAATTATGTTATTCCTGTTACATAACCGGCTAAATATGGC 902
;
; QY 261 ArgTyrLysIleIleLysLeuLeuHisGlyAlaAspMetMetThrLysAsnLeu 280
; DB 903 GATTATGCTGTGATTAATAATTAGTTTATAGACCACTAATAACATAAGCAATAAGTCAAC 962
;
; QY 281 AlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHisAlaLeu 300
; DB 963 AACGGTGTACACCGCTTACATAACGCTATATATATATATATATATATATATATATATAT 1013
;
; QY 301 Glu 301
; DB 1014 GAA 1016
;
; RESULT 9
; US-08-477-459-5
; Sequence 5, Application US/08477459
; Patent No. 6001369
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,459
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2849 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 300..1568
; FEATURE:
; NAME/KEY: CDS

```

LOCATION: complement (1685..2848)
US-08-477-459-5

Alignment Scores:

Pred. No.:	2,74e-15	Length:	2849
Score:	227.00	Matches:	68
Percent Similarity:	44.44%	Conservative:	48
Best Local Similarity:	26.05%	Mismatches:	99
Query Match:	13.41%	Indels:	46
DB:	3	Gaps:	7

US-09-758-593A-1 (1-329) x US-08-477-459-5 (1-2849)

Qy	66	LysThrSerLeuAspLeuArgGluIle	-----AspValGlyGlyLeuAsn	83
Db	297	AAATGCTGTTGATGCGGTACAGAAATCTATTCGGGTGATATATCCCTAGTAGAAAA	356	
Qy	84	LeuIleGluLeuArgLysLysArgLysGlnLysLysArgAspAlaLeuAlaSerHis	103	
Db	357	CTTATA-----AAGAATAAGGTAATTCATCAATATATCT---	392	
Qy	104	GluProProGluProGluIleThrGlyProValAspGluGluThrPheLeuLys	123	
Db	393	-----GTAGAGGAACAACACTCGTTA-----ATAGAC	422	
Qy	124	AlaAlaValGluLysMetLysValIleGluLysPheLeuAlaAspGlySerAla	143	
Db	423	GCTATAAGACCGGAATGCCAAATAGTAGAATCTATTAACACCGGACGCAAGTT	482	
Qy	144	AspThrCysAsp---GlnPheArgThrAlaLeuHisArgAlaSerLeuGluGlyHis	162	
Db	483	AATCATGTAAATFACTAAATCTCTAATCCCTGTTTAAACAGCTATCAAAATAGGATCACAC	542	
Qy	162	-----	162	
Db	543	GATATAGTAAAACTGCTGTGATTAAACGGAGTTGATCTTCTATTTCGCCAGTCCCTGC	602	
Qy	163	-----MetGluIleGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAsp	180	
Db	603	ATAATAAAGAAATGATAAAATCTATATTAGATAGTGTGTAAGTAACACAAAAAT	662	
Qy	181	ArgLeuAspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValLys	200	
Db	663	GCTAAATCTAAACCTTCTGCAATACCGGATTACGAATAAGTAATAGCTTAGAGGTTATCAA	722	
Qy	201	LeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeu	220	
Db	723	ATGCTTTTGTAGTGGCTGATGTTATATAAAGATGATAACATATGTTATCTATA	782	
Qy	221	HisValAlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeu	240	
Db	783	CACATAGCTACTAGGAGTAATCATAGAAATCATAAAAATTTACTATTAGAAAAAGGTGCT	842	
Qy	241	GluIleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsn	260	
Db	843	TATGCAACAGCTAAAGACAAATTTATGTAATCTCCGTTACATAACCGCGCTAAATATGCG	902	
Qy	261	ArgTyrLysIleLeuLysLeuLeuHisGlyAlaAspMetMetThrLysAsnLeu	280	
Db	903	GATTATGCTGTATTAAATGTTTAGACCATCTAATAACATAAGCAATAAGTGCAAC	962	
Qy	281	AlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHisAlaLeu	300	
Db	963	AACGGTGTACACCGGTATACATACCGCTATATAT-----AATAGATCTGCCGTA	1013	
Qy	301	Glu 301		
Db	1014	GAA 1016		

RESULT 10

US-08-479-869-5

; Sequence 5, Application US/08479869

; Patent No. 6123949

GENERAL INFORMATION:
APPLICANT: Cochran Ph.D, Mark D
TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,869
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/024,156
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523

SEQUENCE CHARACTERISTICS:
LENGTH: 2849 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:

NAME/KEY: CDS
LOCATION: 300..1568
FEATURE:
NAME/KEY: CDS
LOCATION: complement (1685..2848)
US-08-479-869-5

Alignment Scores:
Pred. No.: 2,74e-15 Length: 2849
Score: 227.00 Matches: 68
Percent Similarity: 44.44% Conservative: 48
Best Local Similarity: 26.05% Mismatches: 99
Query Match: 13.41% Indels: 46
DB: 3 Gaps: 7

US-09-758-593A-1 (1-329) x US-08-479-869-5 (1-2849)

Qy	66	LysThrSerLeuAspLeuArgGluIle	-----AspValGlyGlyLeuAsn	83
Db	297	AAATGCTGTTGATGCGGTACAGAAATCTATTCGGGTGATATATCCCTAGTAGAAAA	356	
Qy	84	LeuIleGluLeuArgLysLysArgLysGlnLysLysArgAspAlaLeuAlaSerHis	103	
Db	357	CTTATA-----AAGAATAAGGTAATTCATCAATATATCT---	392	
Qy	104	GluProProGluProGluIleThrGlyProValAspGluGluThrPheLeuLys	123	
Db	393	-----GTAGAGGAACAACACTCGTTA-----ATAGAC	422	
Qy	124	AlaAlaValGluLysMetLysValIleGluLysPheLeuAlaAspGlySerAla	143	
Db	423	GCTATAAGACCGGAATGCCAAATAGTAGAATCTATTAACACCGGACGCAAGTT	482	


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; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: PCT/US94/01826A
;
; FILING DATE: 28-FEB-1994
;

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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523

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, ILEX: 422323
, INFORMATION FOR SEQ ID NO: 5:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 2849 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: double
, TOPOLOGY: linear
, MOLECULE TYPE: DNA (genomic)
, HYPOTHETICAL: NO
, ANTI-SENSE: NO
, FEATURE:
,

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Alignment Scores:		
Pred. No.:	2.74e-15	2849
Score:	227.00	Matches: 68
Percent Similarity:	44.44%	Conservative: 48
Best Local Similarity:	26.05%	Mismatches: 99
Query Match:	13.41%	Indels: 46
DR:	5	Gaps: 7

US-09-758-593A-1 (1-329) X PCT-US94-01826A-5 (1-2849)

QY	66	LysThrSerLeuAspLeuArgGluIle	-----AspValGlyGlyIleGlnAsn	83
			:::	
Db	297	AAAATGCTGTTGATGGCGTACAGAAATCTATTTCGGGTGATATATCCCTAGTAGAGAAA	356	
QY	84	LeuIleGluLeuArgLysGlnLysLysArgAspAlaLeuAlaSerHis	103	
			:::	
Db	357	CTTATA	-----AGAAATAAGGTAATGTCATCAATATCT	392
QY	104	GluProProGluProGluIleThrGlyProValAspGluThrPheLeuLys	123	
				:::
Db	393	-----GTAGAGGAAACAACAACCTCCGTTA	-----ATAGAC	422
124	AlaAlaValIGluGlyLysMetLysValIleGluLysPheLeuAlaAspGlyGlySerAla	143		
Db	423	GCATAGAAACCGGAAATGCCAAAATAGTAGAACTATTTTCAAGCAGCGCGCGCAAGTT	482	
QY	144	AspThrCysAsp---GlnPheArgArgThrAlaLeuHisArgAlaSerLeuGluGlyHis	162	
		:::		:::
Db	483	AATCATGTAATACTAAAATTCCTAATCCCTGTTTAAACAGCTATCAAAATAGGATCACAC	542	
QY	162	-----	-----	162
Db	543	GATATAGTAAACGCTGTTGATTACGGAGTTGATCTCTATTTTGGCAGTCCCTCGC	602	
QY	163	-----MetGluIleLeuGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAsp	180	
Db	603	ATAAATAACAACAAATGATAAAACACTATTAGATAGTGGTGTGAAAGTAAACACACAAAAAT	662	
QY	181	ArgLeuAspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLys	200	
Db	663	GCTAAATCTAAAATCTTCTTGCATACCGCGATTAGAAATAATGACTTACGAGGTATACAA	722	
QY	201	LeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeu	220	
Db	723	ATGCTTTTCAGTATGGAGCTGATGTTAATATAAAGAGTAAACATATGTTATTCTATA	782	

Qy	221	HisValAlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuClyLeu	240
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Db	783	CACATAGCTACTAGGAGTAAATTCATATGAATCATATAAATTACTATTAGAAAAGGTGCT	842
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Qy	241	GluTleAsnAlaArgAspArgGluGlyVasprThrAlaLeuHisAspAlaValArgLeuAsn	260
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Db	843	TATGCCAACGGTAAGAACAATTATGGTAATCTCCGTTACATAACCGGCTAAATATGC	902
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Qy	261	ArgThrLysTlleleLysLeuLeuLeuHisGlyAlaAspMetMetThrLysAsnLeu	280
		: : : : : : :	
Db	903	GAUTATCGTGTATTAAATTAGTTTATAGACCAPACTAATAAGCATAAGCAATTAAGTGCAAC	962
		: : : : : : : : : : : : :	
Qy	281	AlaClyLysThrProthrAspLeuValGlnLeuTrpGlnAlaAspThrArqHisAlaLeu	300
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Db	963	AACGGTGTACACCGTTACATACGGCTACTATATAT-----AATGATCTGCCGTA	1013
		: : : : : : : : : : : : :	
Qy	301	Glu 301	
Db	1014	GAA 1016	

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1  RESULT 13
2  PCT-US94-02252A-5
3  ; Sequence 5, Application PC/TUS9402252A
4  ; GENERAL INFORMATION:
5  ; APPLICANT: Syntco Corporation, et al.
6  ; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
7  ; NUMBER OF SEQUENCES: 20
8  ; CORRESPONDENCE ADDRESS:
9  ; ADDRESSEE: John P. White
10 ; STREET: 30 Rockefeller Plaza
11 ; CITY: New York
12 ; STATE: New York
13 ; COUNTRY: USA
14 ; ZIP: 10112
15 ; COMPUTER READABLE FORM:
16 ; MEDIUM TYPE: Floppy disk
17 ; COMPUTER: IBM PC compatible
18 ; OPERATING SYSTEM: PC-DOS/MS-DOS
19 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
20 ; CURRENT APPLICATION DATA:
21 ; APPLICATION NUMBER: PCT/US94/02252A
22 ; FILING DATE: 28-FEB-1994
23 ; CLASSIFICATION:
24 ; ATTORNEY/AGENT INFORMATION:
25 ; NAME: White Esq, John P
26 ; TELECOMMUNICATION INFORMATION:
27 ; TELEPHONE: (212)977-9550
28 ; TELEFAX: (212)664-0525
29 ; TELFX: 422523

```

Alignment Scores:		
Pred. No.:	2,74e-15	2849
Score:	227.00	68
Percent Similarity:	44.44%	Matches: 48
Best local Similarity:	26.03%	Conservative: 99
Query Match:	13.41%	Mismatches: 46
		Indels:


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Db 542 ACGGCTTTTCATGGAAGCTGCTGAGCGTGGTAACGCTGAAGCCTTAAGATTCCTTTTGTCT 601
Qy 149 -----PheArgArg----- 151
Db 602 AAGGAGGCAATGTAATTTGGCGACGACAGACAGCAAGGACAAAGGCGGATTGAAGCAA 661
Qy 152 -----ThrAlaLeuHisArgAlaSerLeuGluGlyHisMetGluIleLeuGluLys 168
Db 662 GGAGCGGCCACAGCTCTCATGAGCGCTCTGAGAGGGCCACCTGGAAGTCTTGAGAAATT 721
Qy 169 LeuLeu----AspAsnGlyAlaThrValAspPheGlnAspArg-----Leu 182
Db 722 CTCCTCAATGACATGAAGCGAAGTCGATGCTCGGGACAACATGGGCGAGAAATGCCCTG 781
Qy 183 AspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLysLeu 202
Db 782 ATCCCTACTCTGCTGAACCTGGAATTTGAAATGTGGAG---GAGATTACTTCAATCCTG 838
Qy 203 GlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeuHisVal 222
Db 839 ATTCAGCAGCGGGCTGATGTTAACTGAGAGGAGAGGAGGAAACACCCCTCATCGCA 898
Qy 223 AlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeu---GlyLeuGlu 241
Db 899 GCAGTGGAGAGGAACACACAGCGCTGTGTCAGATGCTCCTGAGTCGGGGAAGGCATAAAC 958
Qy 242 IleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsnArg 261
Db 959 ATGATGCGCAGGATGAACAGGGCAAGACAGCTCTGCTAAATGCTGTGTGTAACAACTG 1018
Qy 262 TyrIleIleLeuLeuLeuLeuHisGlyAlaAspMetMetLeuLysAsnLeuAla 281
Db 1019 AAGGAAATGTCACGCTGCTCTTCTTAAAGGAGGAGCTGATAAGTGT----- 1063
Qy 282 GlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHis 298
Db 1064 -----GACGATCTTGT-----TGATAGCCAGGAGGAATCAT 1096

RESULT 15
US-08-436-771-5
; Sequence 5, Application US/08436771
; Patent No. 5861300
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: SenGupta, Dibyendu N.
; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
; TITLE OF INVENTION: Cells and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell
; STREET: 200 E. Broward Boulevard
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,771
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,973
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CUI1363-16
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498
; TELEFAX: 305/764/4996
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 164..2200
US-08-436-771-5

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Pred. No.: 4,04e-15 Length: 2200
Score: 224.00 Matches: 89
Percent Similarity: 41.01% Conservativeness: 41
Best Local Similarity: 28.08% Mismatches: 101
Query Match: 13.23% Indels: 86
DB: 2 Gaps: 13

US-09-758-593A-1 (1-329) x US-08-436-771-5 (1-2200)
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Qy 61 GlnGluArgValArgLysThrSerLeuAspLeuArgGluIleIleAspValGlyGly 80
Db 269 GGAGATGTTGTCAAGGTC-----CAGCAATTTGTAGAAAAAGGGCT 310
Qy 81 IleGlnAsnLeuIleGlu-----LeuArgLysLysArgLysGln 93
Db 311 GATGCCAATGCTGTGAAGACACCTGGGGCTGGACACCTTTGCACACGCGAGTGCAGCT 370
Qy 94 LysLysArgAspAla-----LeuAlaAlaSerHisGluProProGluProGluGlu 111
Db 371 GGCAGGGTAGACATGTGAACCTCTCTGCTGTAGTCATGCTGTGACCTCATCGGAGGA 430
Qy 112 IleThrGlyProValAspGluThrPheLeuLysAlaAlaValGluGlyLysMetLys 131
Db 431 AAGAATGGGGCCACC-----CCCTTCATCATTTGCTGGGATCCAGGGAGATGTGAAA 481
Qy 132 ValIleGluLysPheLeuAlaAspGlySerAlaAspThrCysAspGln----- 148
Db 482 CTGCTCGAGATTCCTCTCTTGTGGTCACAGCTCAATGAGTGTGACGAGAACGGATTTC 541
Qy 148 -----LeuArgLysLysArgLysGln 148
Db 542 ACGGCTTTTCATGGAAGCTGCTGAGCGTGGTAACGCTGAAGCCTTAAGATTCCTTTTGTCT 601
Qy 149 -----PheArgArg----- 151
Db 602 AAGGAGGCAATGTCAATTTTCGACGACAGACAGCAAGGACAAAGGCGGATTGAAGCAA 661
Qy 152 -----ThrAlaLeuHisArgAlaSerLeuGluGlyHisMetGluIleLeuGluLys 168
Db 662 GGAGCGGCCACAGCTCTCATGAGCGCTCTGAGAGGGCCACCTGGAAGTCTTGAGAAATT 721
Qy 169 LeuLeu----AspAsnGlyAlaThrValAspPheGlnAspArg-----Leu 182
Db 722 CTCCTCAATGACATGAAGCGAAGTCGATGCTCGGGACAACATGGGCGAGAAATGCCCTG 781
Qy 183 AspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLysLeu 202
Db 782 ATCCCTACTCTGCTGAACCTGGAATTTGAAATGTGGAG---GAGATTACTTCAATCCTG 838
Qy 203 GlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeuHisVal 222
Db 839 ATTCAGCAGCGGGCTGATGTTAACTGAGAGGAGAGGAGGAAACACCCCTCATCGCA 898
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Qy	223	AlaValArgThrGlyGlnValGluLeuValGluHisPheLeuSerLeu---	GlyLeuGlu	241
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Qy	242	IleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsnArg		261
Db	959	ATGATATGCCAGGGATAACAGGGCAAGACAGCTCTGTAATTGCTGTGTGATAACAACATG		1018
Qy	262	TyrLysIleLeuLysLeuLeuLeuLeuHisGlyAlaAspMetMetThrLysAsnLeuAla		281
Db	1019	AAGGAATATTGCCAGTGTGCTCTTGGAAAGGAGCTGATAAGTCT	-----	1063
Qy	282	GlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHis		298
Db	1064	-----GAGCATCTTGT-----TCGATACCGAGGAGGAATCAT		1096

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Job time : 87 secs

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